



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/265,120  
Source: IFWO  
Date Processed by STIC: 9/1/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

~~TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE~~ CHECKER  
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/efb/efs/downloads/documents.htm>) , EFS Submission User Manual - cPAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10765,120

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos        was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will  
                               prevent "wrapping."
  
- 2      Invalid Line Length    The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3   J   Misaligned Amino    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers;  
     Numbering                use **space characters**, instead.
  
- 4      Non-ASCII            The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please  
                               ensure **your subsequent submission is saved in ASCII text**.
  
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. **Per Sequence Rules,**  
                               each n or Xaa can only represent a single residue. Please present the **maximum** number of each  
                               residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0        A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"                    sequences(s)             . Normally, PatentIn would automatically generate this section from the  
                               previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
                               the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for**  
                               **Artificial or Unknown sequences.**
  
- 7      Skipped Sequences    Sequence(s)      missing. If intentional, please insert the following lines for **each** skipped sequence:  
     (OLD RULES)            (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               (i)        SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                               (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               This sequence is intentionally skipped  
  
                               Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8      Skipped Sequences    Sequence(s)      missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
     (NEW RULES)            <210> sequence id number  
                               <400> sequence id number  
                               000
  
- 9      Use of n's or Xaa's    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)            Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                               In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10      Invalid <213>        Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or  
     Response                scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or  
                               is Artificial Sequence
  
- 11      Use of <220>        Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
                               Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or  
                               "Unknown." Please explain source of genetic material in <220> to <223> section.  
                               (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0        Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"                    resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                               listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n/Xaa      "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/765,120

DATE: 09/01/2004

TIME: 12:45:36

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\09012004\J765120.raw

1 <110> APPLICANT: Benner, Steven Albert  
W--> 2 <120> TITLE OF INVENTION: Evolution-Based Functional Genomics  
W--> 3 <140> CURRENT APPLICATION NUMBER: 10/765,120  
W--> 0 <130> FILE REFERENCE:  
4 <141> CURRENT FILING DATE: 2004-01-28  
W--> 5 <160> NUMBER OF SEQ ID: 38  
6 <170> SOFTWARE: MacIntosh OS 10.3 Microsoft Word v. 2003

## ERRORED SEQUENCES

938 <210> SEQ ID NO: 14  
939 <211> LENGTH: 478  
940 <212> TYPE: PRT  
941 <213> ORGANISM: Oryctolagus cuniculus  
W--> 942 <400> SEQUENCE: 14  
E--> 943 Met Leu Leu Glu Val Leu Asn Pro Arg His Tyr Asn Val Thr Ser  
944 ~~005~~ 5 ~~010~~ 10 ~~015~~ 15  
945 Met Val Ser Glu Val Val Pro Ile Ala Ser Ile Ala Ile Leu Leu  
946 ~~020~~ 20 ~~025~~ 25 ~~030~~ 30  
947 Leu Thr Gly Phe Leu Leu Leu Val Trp Asn Tyr Glu Asp Thr Ser  
948 ~~035~~ 35 ~~040~~ 40 ~~045~~ 45  
949 Ser Ile Pro Gly Pro Ser Tyr Phe Leu Gly Ile Gly Pro Leu Ile  
950 ~~050~~ 50 ~~055~~ 55 ~~060~~ 60  
951 Ser His Cys Arg Phe Leu Trp Met Gly Ile Gly Ser Ala Cys Asn  
952 ~~065~~ 65 ~~070~~ 70 ~~075~~ 75  
953 Tyr Tyr Asn Lys Met Tyr Gly Glu Phe Met Arg Val Trp Val Cys  
954 ~~080~~ 80 ~~085~~ 85 ~~090~~ 90  
955 Gly Glu Glu Thr Leu Ile Ile Ser Lys Ser Ser Ser Met Phe His  
956 ~~095~~ 95 100  
957 Val Met Lys His Ser His Tyr Ile Ser Arg Phe Gly Ser Lys Leu  
958 110 115 120  
959 Gly Leu Gln Phe Ile Gly Met His Glu Lys Gly Ile Ile Phe Asn  
960 125 130 135  
961 Asn Asn Pro Ala Leu Trp Lys Ala Val Arg Pro Phe Phe Thr Lys  
962 140 145 150  
963 Ala Leu Ser Gly Pro Gly Leu Val Arg Met Val Thr Ile Cys Ala  
964 155 160 165  
965 Asp Ser Ile Thr Lys His Leu Asp Arg Leu Glu Glu Val Cys Asn  
966 170 175 180  
967 Asp Leu Gly Tyr Val Asp Val Leu Thr Leu Met Arg Arg Ile Met  
968 185 190 195  
969 Leu Asp Thr Ser Asn Met Leu Phe Leu Gly Ile Pro Leu Asp Glu

pp1-7  
Does Not Comply  
Corrected Diskette Needed

← misaligned  
amino acid  
numbers  
(see item 3  
on error  
summary  
sheet)

Please delete  
0's (zeros)  
before two-digit  
amino acid numbers.

(see sample  
Sequence Listing  
attached in back,  
for example)

also, see 1-822 of  
Sequence Rules

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/765,120

DATE: 09/01/2004

TIME: 12:45:36

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\09012004\J765120.raw

```

970          200          205          210
971 Ser Ala Ile Val Val Asn Ile Gln Gly Tyr Phe Asp Ala Trp Gln
972          215          220          225
973 Ala Leu Leu Leu Lys Pro Asp Ile Phe Phe Lys Ile Ser Trp Leu
974          230          235          240
975 Cys Arg Lys Tyr Glu Lys Ser Val Lys Asp Leu Lys Asp Ala Met
976          245          250          255
977 Glu Ile Leu Ile Ala Glu Lys Arg His Arg Ile Ser Thr Ala Glu
978          260          265          270
979 Lys Leu Glu Asp Ser Ile Asp Phe Ala Thr Glu Leu Ile Phe Ala
980          275          280          285
981 Glu Lys Arg Gly Glu Leu Thr Arg Glu Asn Val Asn Gln Cys Ile
982          290          295          300
983 Leu Glu Met Leu Ile Ala Ala Pro Asp Thr Met Ser Val Ser Val
984          305          310          315
985 Phe Phe Met Leu Phe Leu Ile Ala Lys His Pro Gln Val Glu Glu
986          320          325          330
987 Ala Ile Ile Arg Glu Ile Gln Thr Val Val Gly Glu Arg Asp Ile
988          335          340          345
989 Arg Ile Asp Asp Met Gln Lys Leu Lys Val Val Glu Asn Phe Ile
990          350          355          360
991 Asn Glu Ser Met Arg Tyr Gln Pro Val Val Asp Leu Val Met Arg
992          365          370          375
993 Lys Ala Leu Glu Asp Asp Val Ile Asp Gly Tyr Pro Val Lys Lys
994          380          385          390
995 Gly Thr Asn Ile Ile Leu Asn Leu Gly Arg Met His Arg Leu Glu
996          395          400          405
997 Phe Phe Pro Lys Pro Asn Glu Phe Thr Leu Glu Asn Phe Ala Lys
998          410          415          420
999 Asn Val Pro Tyr Arg Tyr Phe Gln Pro Phe Gly Phe Gly Pro Arg
1000          425          430          435
1001 Gly Cys Ala Gly Lys Tyr Ile Ala Met Val Met Met Lys Val Val
1002          440          445          450
1003 Leu Val Thr Leu Leu Arg Arg Phe His Val Gln Thr Leu Gln Gly
1004          455          460          465
1005 Arg Cys Val Glu Lys Met Gln Lys Lys Asn Asp Leu Ser Leu His
1006          470          475          480
1007 Pro Asp Glu Thr Arg Asp

```

E--&gt; 1008

485

1151 &lt;210&gt; SEQ ID NO: 17

1152 &lt;211&gt; LENGTH: 486

1153 &lt;212&gt; TYPE: PRT

1154 &lt;213&gt; ORGANISM: Poephila guttata

W--&gt; 1155 &lt;400&gt; SEQUENCE: 17

```

1156 Met Phe Leu Glu Met Leu Asn Pro Met His Tyr Asn Val Thr Ile
1157          405          410          415
1158 Met Val Pro Glu Thr Val Pro Val Ser Ala Met Pro Leu Leu Leu
1159          420          425          430
1160 Ile Met Gly Leu Leu Leu Leu Ile Arg Asn Cys Glu Ser Ser Ser

```

*see p.3, too*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/765,120

DATE: 09/01/2004

TIME: 12:45:36

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\09012004\J765120.raw

1161		035		040		045									
1162	Ser	Ile	Pro	Gly	Pro	Gly	Tyr	Cys	Leu	Gly	Ile	Gly	Pro	Leu	Ile
1163				050		055								060	
1164	Ser	His	Gly	Arg	Phe	Leu	Trp	Met	Gly	Ile	Gly	Ser	Ala	Cys	Asn
1165				065		070								075	
1166	Tyr	Tyr	Asn	Lys	Met	Tyr	Gly	Glu	Phe	Met	Arg	Val	Trp	Ile	Ser
1167				080		085								090	
1168	Gly	Glu	Glu	Thr	Leu	Ile	Ile	Ser	Lys	Ser	Ser	Ser	Met	Val	His
1169				095		100								105	
1170	Val	Met	Lys	His	Ser	Asn	Tyr	Ile	Ser	Arg	Phe	Gly	Ser	Lys	Arg
1171				110		115								120	
1172	Gly	Leu	Gln	Cys	Ile	Gly	Met	His	Glu	Asn	Gly	Ile	Ile	Phe	Asn
1173				125		130								135	
1174	Asn	Asn	Pro	Ser	Leu	Trp	Arg	Thr	Val	Arg	Pro	Phe	Phe	Met	Lys
1175				140		145								150	
1176	Ala	Leu	Thr	Gly	Pro	Gly	Leu	Ile	Arg	Met	Val	Glu	Val	Cys	Val
1177				155		160								165	
1178	Glu	Ser	Ile	Lys	Gln	His	Leu	Asp	Arg	Leu	Gly	Asp	Val	Thr	Asp
1179				170		175								180	
1180	Asn	Ser	Gly	Tyr	Val	Asp	Val	Val	Thr	Leu	Met	Arg	His	Ile	Met
1181				185		190								195	
1182	Leu	Asp	Thr	Ser	Asn	Thr	Leu	Phe	Leu	Gly	Ile	Pro	Leu	Asp	Glu
E--> 1183				<del>200</del> 200		<del>205</del> 205							<del>210</del> 210		
1184	Ser	Ser	Ile	Val	Lys	Lys	Ile	Gln	Gly	Tyr	Phe	Asn	Ala	Trp	Gln
E--> 1185				215		220								225	
1186	Ala	Leu	Leu	Ile	Lys	Pro	Asn	Ile	Phe	Phe	Lys	Ile	Ser	Trp	Leu
E--> 1187				230		235								240	
1188	Tyr	Arg	Lys	Tyr	Glu	Arg	Ser	Val	Lys	Asp	Leu	Lys	Asp	Glu	Ile
E--> 1189				245		250								255	
1190	Glu	Ile	Leu	Val	Glu	Lys	Lys	Arg	Gln	Lys	Val	Ser	Ser	Ala	Glu
E--> 1191				260		265								270	
1192	Lys	Leu	Glu	Asp	Cys	Met	Asp	Phe	Ala	Thr	Asp	Leu	Ile	Phe	Ala
E--> 1193				275		280								285	
1194	Glu	Arg	Arg	Gly	Asp	Leu	Thr	Lys	Glu	Asn	Val	Asn	Gln	Cys	Ile
E--> 1195				290		295								300	
1196	Leu	Glu	Met	Leu	Ile	Ala	Ala	Pro	Asp	Thr	Met	Ser	Val	Thr	Leu
E--> 1197				305		310								315	
1198	Tyr	Val	Met	Leu	Leu	Leu	Ile	Ala	Glu	Tyr	Pro	Glu	Val	Glu	Thr
E--> 1199				320		325								330	
1200	Ala	Ile	Leu	Lys	Glu	Ile	His	Thr	Val	Val	Gly	Asp	Arg	Asp	Ile
E--> 1201				335		340								345	
1202	Arg	Ile	Gly	Asp	Val	Gln	Asn	Leu	Lys	Val	Val	Glu	Asn	Phe	Ile
E--> 1203				350		355								360	
1204	Asn	Glu	Ser	Leu	Arg	Tyr	Gln	Pro	Val	Val	Asp	Leu	Val	Met	Arg
E--> 1205				365		370								375	
1206	Arg	Ala	Leu	Glu	Asp	Asp	Val	Ile	Asp	Gly	Tyr	Pro	Val	Lys	Lys
E--> 1207				380		385								390	
1208	Gly	Thr	Asn	Ile	Ile	Leu	Asn	Ile	Gly	Arg	Met	His	Arg	Leu	Glu
E--> 1209				395		400								405	

← misaligned  
amino acid  
numbers

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/765,120

DATE: 09/01/2004

TIME: 12:45:36

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\09012004\J765120.raw

1210 Tyr Phe Pro Lys Pro Asn Glu Phe Thr Leu Glu Asn Phe Glu Lys  
 E--> 1211 410 415 420  
 1212 Asn Val Pro Tyr Arg Tyr Phe Gln Pro Phe Gly Phe Gly Pro Arg  
 E--> 1213 425 430 435  
 1214 Ser Cys Ala Gly Lys Tyr Ile Ala Met Val Met Met Lys Val Val  
 E--> 1215 440 445 450  
 1216 Leu Val Thr Leu Leu Lys Arg Phe His Val Lys Thr Leu Gln Lys  
 E--> 1217 455 460 465  
 1218 Arg Cys Ile Glu Asn Met Pro Lys Asn Asn Asp Leu Ser Leu His  
 E--> 1219 470 475 480  
 1220 Leu Asp Glu Asp Ser Pro  
 E--> 1221 485

1445 <210> SEQ ID NO: 35  
 1446 <211> LENGTH: 83  
 1447 <212> TYPE: DNA  
 1448 <213> ORGANISM: Sus scrofa  
 W--> 1449 <400> SEQUENCE: 35

C--> 1450 caatcattac acgtgccgat ttggcagcaa acctggggttg gaatgcattg gcatgcatga 60  
 E--> 1451 aaaaggcatca tggttaacaa taa

1453 <210> SEQ ID NO: 36

1454 <211> LENGTH: 84

1455 <212> TYPE: DNA

1456 <213> ORGANISM: Sus scrofa

W--> 1457 <400> SEQUENCE: 36

C--> 1458 tagtcactac acatcccgat ttggcagcaa acctggggttg cagttcattg gcatgcatga 60

E--> 1459 gaaaggcatt atattcaaca ataa

1461 <210> SEQ ID NO: 37

1462 <211> LENGTH: 84

1463 <212> TYPE: DNA

1464 <213> ORGANISM: Sus scrofa

W--> 1465 <400> SEQUENCE: 37

C--> 1466 cagtcactac acatcccgat tcggcagcaa acctggggttg gagtgcacgc gcatgtatga 60

E--> 1467 gaagggcatc atatttaata atga

E--> 1469 <210> SEQ ID NO: 37 38 ← change to

1470 <211> LENGTH: 84

1471 <212> TYPE: DNA

1472 <213> ORGANISM: White lipped peccary

W--> 1473 <400> SEQUENCE: 37 38 ← change to

C--> 1474 cagtcactac acatcccgat tcggcagcaa acctggggttg cagttcattg gaatgcattg 60

E--> 1475 gaaaggcatc atatttaaca acaa

IMPORTANT: use lower-case letters  
for nucleotides

84 ← insert  
 cumulative  
 base total  
 at right  
 margin  
 of each  
 line

84  
 ↑  
 insert

84 ← insert

84 ← insert

10/765,120 5

<210> 26

<211> 50

<212> PRT

<213> Ancestral sequence

<400> 26

Arg Asn Val Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp  
005 010 015  
Leu Leu His Leu Leu Ala Ser Ser Lys Ser Cys Pro Leu Pro Gln  
020 025 030  
Ala Arg Gly Leu Glu Thr Leu Glu Ser Leu Gly Gly Val Leu Glu  
035 040 045  
Ala Ser Leu Tyr Ser  
050

invalid <213> response. see item 10 on

Even summary

sheet.

6

Please  
consult

<110> Smith, John; Smithgene Inc.

<120> Example of a Sequence Listing

<130> 01-00001

<140> PCT/EP98/00001

<141> 1998-12-31

<150> US 08/999,999

<151> 1997-10-15

<160> 4

<170> PatentIn version 2.0

<210> 1

<211> 389

<212> DNA

<213> Paramecium sp.

<220>

<221> CDS

<222> (279)...(389)

<300>

<301> Doe, Richard

<302> Isolation and Characterization of a Gene Encoding a  
Protease from Paramecium sp.

<303> Journal of Genes

<304> 1

<305> 4

<306> 1-7

<307> 1988-06-31

<308> 123456

<309> 1988-06-31

<400> 1

agctgtagtc	attcctgtgt	cctctttctct	ctgggcttct	caccctgcta	atcagatctc	60
agggagagtg	tcttgaccct	cctctgcctt	tgcagcttca	caggcaggca	ggcaggcagc	120
tgatgtggca	attgctggca	gtgccacagg	cttttcagcc	aggcttaggg	tgggttccgc	180
cgcggcgcg	cggccctct	cgcgctctc	tgcgctct	ctctcgctct	cctctcgctc	240



7

```

ggacctgatt  aggtgagcag  gaggaggggg  cagtttagc      atg  gtt  tca  atg  ttc  agc  296
Met  Val  Ser  Met  Phe  Ser
1      5

ttg  tct  ttc  aaa  tgg  cct  gga  ttt  tgt  ttg  ttt  gtt  tgt  ttg  ttc  caa  344
Leu  Ser  Phe  Lys  Trp  Pro  Gly  Phe  Cys  Leu  Phe  Val  Cys  Leu  Phe  Gln
10      15      20

tgt  ccc  aaa  gtc  ctc  ccc  tgt  cac  tca  tca  ctg  cag  ccg  aat  ctt  389
Cys  Pro  Lys  Val  Leu  Pro  Cys  His  Ser  Ser  Leu  Gln  Pro  Asn  Leu
25      30      35

<210>      2
<211>      37
<212>      PRT
<213>      Paramecium sp.

<400>      2
Met  Val  Ser  Met  Phe  Ser  Leu  Ser  Phe  Lys  Trp  Pro  Gly  Phe  Cys  Leu
1      5      10

Phe  Val  Cys  Leu  Phe  Gln  Cys  Pro  Lys  Val  Leu  Pro  Cys  His  Ser  Ser
20      25      30

Leu  Gln  Pro  Asn  Leu
35

<210>      3
<211>      11
<212>      PRT
<213>      Artificial Sequence

<220>
<223>      Designed peptide based on size and polarity to act as a
linker between the alpha and beta chains of Protein XYZ.

<400>      3
Met  Val  Asn  Leu  Glu  Pro  Met  His  Thr  Glu  Ile
1      5      10

<210>      4
<400>      4
000

```

[Annex VIII follows]

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/765,120

DATE: 09/01/2004

TIME: 12:45:37

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\09012004\J765120.raw

L:2 M:283 W: Missing Blank Line separator, <120> field identifier  
 L:3 M:283 W: Missing Blank Line separator, <140> field identifier  
 L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE  
 L:5 M:283 W: Missing Blank Line separator, <160> field identifier  
 L:12 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:84 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:156 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:228 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:300 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:371 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:443 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:515 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:585 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:656 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:728 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:800 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:872 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:942 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:944 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14  
 L:1008 M:252 E: No. of Seq. differs, <211> LENGTH:Input:478 Found:486 SEQ:14  
 L:1014 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1086 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1155 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1183 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1185 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1187 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1189 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1191 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1193 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1195 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1197 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1199 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1201 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1203 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1205 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1207 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1209 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1211 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1213 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1215 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1217 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1219 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1221 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
 L:1227 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1241 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1255 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1269 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1283 M:283 W: Missing Blank Line separator, <400> field identifier

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/765,120

DATE: 09/01/2004

TIME: 12:45:37

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\09012004\J765120.raw

L:1297 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1311 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1325 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1339 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1353 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1367 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1381 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1395 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1409 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1419 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1429 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1439 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1449 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1450 M:112 C: (48) String data converted to lower case,  
L:1451 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:84 SEQ:35  
L:1451 M:112 C: (48) String data converted to lower case,  
L:1451 M:252 E: No. of Seq. differs, <211> LENGTH:Input:83 Found:84 SEQ:35  
L:1457 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1458 M:112 C: (48) String data converted to lower case,  
L:1459 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:84 SEQ:36  
L:1459 M:112 C: (48) String data converted to lower case,  
L:1465 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1466 M:112 C: (48) String data converted to lower case,  
L:1467 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:84 SEQ:37  
L:1467 M:112 C: (48) String data converted to lower case,  
L:1469 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO:37  
L:1473 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1474 M:112 C: (48) String data converted to lower case,  
L:1475 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:84 SEQ:37  
L:1475 M:112 C: (48) String data converted to lower case,